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<b>AMENDMENT TRANSMITTAL</b>		Docket No. B0004/7514
Applicant:	Felix Hausch and Andres Jäschke	
Serial No:	09/817,905	
Filed:	March 26, 2001	
For:	MULTIPLEX SEQUENCE VARIATION ANALYSIS OF DNA SAMPLES BY MASS SPECTROMETRY	
Examiner:	A. K. Chakrabarti	
Art Unit:	1634	

Assistant Commissioner for Patents  
Washington, D.C. 20231

Transmitted herewith for filing is the following:

**Enclosures**

- ☒ Amendment  
☒ Petition for a 1 month Extension of Time  
☒ Return Receipt Postcard  
☐ Other:

**Small Entity**

- ☐ Applicant/assignee claims small entity status.  
☐ Small entity status is no longer claimed.

**Fees**

Claims as Filed					
	Claims Filed	Highest Number Paid for	Number of Extra Claims	Rate	Additional Fees Due
Total Claims (37 CFR §1.16(c))	35	- 35 =	0 X	\$18.00 =	\$ 0.00
Independent Claims (37 CFR §1.16(b))	1	- 3 =	0 X	\$84.00 =	\$ 0.00
Extension Fee					\$ 110.00
Reduction by 50% for filing by small entity					\$ 0.00
Total Filing Fee					<u>\$ 110.00</u>

**Payment**

- ☒ Check in the amount of the total filing fee.  
☐ Charge Account No. in the amount of the total filing fee. A duplicate of this transmittal sheet is attached.

**Authorization to Charge Additional Fees**

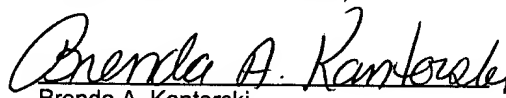
- ☒ The Commissioner is hereby authorized to charge any additional fees under 37 C.F.R. §1.16 and §1.17 required by the attached paper and during the entire pendency of this application to Account No. 02-3038.

Philip L. Conrad Date: April 9, 2003  
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CERTIFICATE OF MAILING UNDER 37 C.F.R. §1.8(a)  
The undersigned hereby certifies that this document is being placed in the United States mail with first-class postage attached, addressed to Assistant Commissioner for Patents, Washington, D.C. 20231 on April 9, 2003.

  
Brenda A. Kantorski

Assistant Commissioner for Patents  
Washington, D.C. 20231

**In response to the office communication dated December 9, 2002, please amend the above-identified application as follows:**

**Substitute Claims**

Please substitute the following claims for pending claims with the same numbers.

1. A method for the analysis of a sample of genetic material for detailed sequence information contained in a large set of distinct sequences of the sample (the "target sequences"),  
comprising the following steps:
  - (1) producing an amount of nucleic acid templates containing the target sequences by multiplexed amplification of the sample of genetic material,
  - (2) using a chip with spatially separated locations containing a photocleavable oligonucleotide probe each for each target sequence to be investigated, the probes covalently bound to the chip surface,
  - (3) modifying, in a single reaction vessel and by using the templates produced in